

```

ORIGIN
Query Match      7.3%; Score 411.8; DB 6; Length 868;
Best Local Similarity 97.6%; Pred. No. 2.2e-94;
Matches 439; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

3645 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 3704
|||||
415 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 474
|||||
3705 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3764
|||||
475 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 534
|||||
3765 CAAATTGTAATTTTGTATCTTCCACTGATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3824
|||||
535 CAAATTGTAATTTTGTATCTTCCACTGATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 594
|||||
3825 TTCAAGCAAA--GCAAAAAACAACCTCCTGGTATCAACAGTATAGCATATTTCAAGATGA 3882
|||||
595 TTCAAGCAAGGGGGGAGACAACCTTCGGTATCAACAGTATAGCATATTTCAAGATGA 654
|||||
3883 GGTGCACTGCTTGTATAGTTGTTATTTAGTCGCAAAATATGTGCAAGTAAGTGGCACT 3942
|||||
655 GGTGCACTGCTTGTATAGTTGTTATTTAGTCGCAAAATATGTGCAAGTAAGTGGCACT 714
|||||
3943 TGAGCCATTAGCTCTCTTAGGATATAGCCAGAGATCGTGTATATAGCTGTGCAAGACA 4002
|||||
715 TGAGCCATTAGCTCTCTTAGGATATAGCCAGAGATCGTGTATATAGCTGTGCAAGACA 774
|||||
4003 CTGTTTTCACCAATTTATATATAGCTGCAATGTTTACATGATGAAGCTTGAATAGGA 4062
|||||
775 CTGTTTTCACCAATTTATATATAGCTGCAATGTTTACATGATGAAGCTTGAATAGGA 834
|||||
4063 TATGGGATGAGTGCAACTGCTGGAGATAGC 4092
|||||
835 TATGGGATGAGTGCC-ACTGCTGGAGATACC 863
|||||

RESULT 11
A1374506/c 871 bp mRNA linear EST 21-JAN-1999
LOCUS MEST6-D3.POLYT-N.Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA
DEFINITION sequence.
ACCESSION A1374506
VERSION A1374506.1 GI:4174526
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 871)
Wen, T.J., Ashlock, D.A. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
Iowa State University
G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: tw1412 (5'-GAAGATACCCCAACCAACC-3')
BACKWARD: T7-YJ (5'-TAATACCACTCACTATAGGC-3')
Plate: MEST6 row: D column: 3
Seq primer: POLYT-N (5'-TTTTTTTTTTTTTTTTTTTTTTT (AGC)-3').
Location/Qualifiers
1..871
/organism="Zea mays"
/mol_type="mRNA"

FEATURES
source
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST6-D3"
/tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XLI-MFR Blue"
/clone_lib="ISUM2"
/notes="Organ: green seedlings; Vector: PAD-GAL4; Site 1:
ECORI; Site 2: XhoI; ds-cDNA molecules were generated as
follows. First-strand cDNA was prepared from oligo-dT
selected mRNA by priming with an XhoI oligo-dT primer. The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcorI adaptors, the
ds-cDNAs were digested with XhoI and size-selected. The
resulting molecules were directionally cloned into the
ECORI and XhoI sites of the HybriZAP lambda vector
(Stratagene) and excised as PAD-GAL4 phagemids."
ORIGIN
Query Match      7.3%; Score 410; DB 1; Length 871;
Best Local Similarity 99.5%; Pred. No. 6.4e-94;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

3645 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 3704
|||||
428 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 369
|||||
3705 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3764
|||||
368 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 309
|||||
3765 CAAATTGTAATTTTGTATCTTCCACTGATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3824
|||||
308 CAAATTGTAATTTTGTATCTTCCACTGATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 249
|||||
3825 TTCAAGCAAGCAAAACAACCTCCTGGTATCAACAGTATAGCATATTTCAAGATGAGG 3884
|||||
248 TTCAAGCAAGCAAAACAACCTCCTGGTATCAACAGTATAGCATATTTCAAGATGAGG 189
|||||
3885 TGCACCTGCTTATAGTTGTTATTTAGTCGCAATATGTCAGATGAGTGGCCTTG 3944
|||||
188 TGCACCTGCTTATAGTTGTTATTTAGTCGCAATATGTCAGATGAGTGGCCTTG 129
|||||
3945 AGCATTAGCTCCTCTTAGGATATGGCAGCAGATCGTGTATATAGCTGTGCAAGACACT 4004
|||||
128 AGCATTAGCTCCTCTTAGGATATGGCAGCAGATCGTGTATATAGCTGTGCAAGACACT 69
|||||
4005 GTTTTGCAACCAATTTATATATAGACTGCATTGTTTACATGATGAAGCTTGAATAGGATA 4064
|||||
68 GTTTTGCAACCAATTTATATATAGACTGCATTGTTTACATGATGAAGCTT-AAATAGGATA 10
|||||
4065 TGG 4067
|||||
9 TGG 7
|||||

RESULT 12
CW239849/c 685 bp DNA linear GSS 30-OCT-2004
LOCUS 104.698.11217883.116.37521.076 Sorghum methylation filtered library
DEFINITION (LibID: 104) sorghum bicolor genomic clone 11217883, genomic survey
sequence.
ACCESSION CW239849
VERSION CW239849.1 GI:54948676
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 685)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,

```

Db 459 GGTTCGGGTGACGGAGGGGCAAGATCGTGGCGGTGGCGGGAGGAGCAGCACCTGC 400  
Qy 361 TCGCCAGAGAACACCAAGCGGCAAGAGAGGCTCTCGAAGATGGTCAAGTCAACAGA 420  
Db 399 TCGCCAGAGAACACCAAGCGGCAAGAGAGGCTCTCGAAGATGGTCAAGTCAACAGA 340  
Qy 421 GTGACTAGCAAGTGTACGGGTGCACCTGCCCTACCTCAAGTGAATAGGAAGCAACT 480  
Db 339 GTGACTAGCAAGTGTACGGGTGCACCTGCCCTACCTCAAGTGAATAGGAAGCAACT 280  
Qy 481 GAGAGCTACGTGGTCTTCAAAAAATCATTAAGTTTCGTTCCACCAAAATTTGAATTTGTG 540  
Db 279 GAGAGCTACGTGGTCTTCAAAAAATCATTAAGTTTCGTTCCACCAAAATTTGAATTTGTG 220  
Qy 541 TATCTTCACGTGATTTCTTCAAAAAATCATTAAGTGAATAGGAAGCAACT 600  
Db 219 TATCTTCACGTGATTTCTTCAAAAAATCATTAAGTGAATAGGAAGCAACT 160  
Qy 601 ACACTCCTGGTATCAACAGTATAGCATATTTTCAAGTGAATAGGAAGCAACT 660  
Db 159 ACACTCCTGGTATCAACAGTATAGCATATTTTCAAGTGAATAGGAAGCAACT 100  
Qy 661 TTGTTATTTAGTCCCAATATGTGCAAGTGAATAGGTCGCTGATAGGTCGCTGCTCTT 720  
Db 99 TTGTTATTTAGTCCCAATATGTGCAAGTGAATAGGTCGCTGATAGGTCGCTGCTCTT 44  
Qy 721 AGGATATGGCCAGCAGATCGTGTATATGGCTGTGCAAGCACT 763  
Db 43 AGGATATGGCCAGCAGATCGTGTATATGGCTGTGCAAGCACT 1

RESULT 3  
AI374506/c  
LOCUS  
DEFINITION  
MEST6-D3. POLYT-N. Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
AI374506  
AI374506.1 GI:4174526

ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Wen, T. J., Ashlock, D. A. and Schnable, P. S.  
Expressed Sequence Tags from B73 Maize Seedlings  
Unpublished (1997)  
Contact: Schnable, PS  
Schnable Laboratory  
Iowa State University  
G405 Agronomy, Ames, IA 50011, USA  
Tel: (515)-294-0975  
Fax: (515)-294-2299  
Email: schnable@iastate.edu

PCR Primers  
FORWARD: twi412 (5'-GAAGATACCCCAACCAACC-3')  
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGC-3')  
Plate: MEST6 row: D column: 3  
Seq primer: POLYT-N (5'-TTTTTTTTTTTTTTTTTTTTTTT (AGC)-3').  
Location/Qualifiers  
1. .871  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="MEST6-D3"  
/issue\_type="above ground tissues"  
/dev\_stage="two-leaf-stage green seedling"  
/lab\_host="XL1-MPR Blue"  
/clone\_lib="ISUM2"  
/notes="Organ: green seedlings; Vector: PAD-GAL4; Site 1:  
EcoRI; Site 2: XhoI; ds-cDNA molecules were generated as

FEATURES  
source

follows. First-strand cDNA was prepared from oligo-dT  
selected mRNA by priming with an XhoI oligo-dT primer. The  
resulting DNA:RNA hybrid was treated with RNase H and used  
as a template for DNA PolI-catalyzed second strand  
synthesis. After the addition of EcoRI adaptors, the  
ds-cDNAs were digested with XhoI and size-selected. The  
resulting molecules were directionally cloned into the  
EcoRI and XhoI sites of the HybriZAP lambda vector  
(Stratagene) and excised as pAD-GAL4 phagemids."

ORIGIN  
Query Match 80.7%; Score 672; DB 1; Length 871;  
Best Local Similarity 96.7%; Pred. No. 1.3e-162;  
Matches 703; Conservative 0; Mismatches 22; Indels 2; Gaps 2;  
Qy 100 CCGCGCAGGAGCCAGGAAGCTACCCGACGACGCTCGCATTCGCCGCGAAATCTCTCT 159  
Db 731 CCGCGGCAGNAGCAGGAAGTACCC-CAGCCAGCCTNGCATTCGCCGGGAATCTCTTT 673  
Qy 160 TCGCGCGCCGCTGGCGCCGACCGCGCTCCGTCGCGTCCGCTCCCGCGCAAGCGG 219  
Db 672 TGGGNGCGCGCTTGGCGCCGACCGCGCTTCNGTGGGTGCGCGTCCCGCGCAAGCGG 613  
Qy 220 CCACCTCCACCACTCGCTCGAGGTGTCGCGGGGGGAGAGGGCTACAGATGAAGA 279  
Db 612 CCACCTCCACCACTTCGTTAGAGGTGTCGCGCGGGGAGAGGGGTACAGATGAAGA 553  
Qy 280 CGCACAGGGCGTCGGCGAAGCGGTTCCGGGTGACGGGGAGGGCAAGATCGTGGCGG 339  
Db 552 CGCACAGGGCGTCGGCGAAGCGGTTCCGGGTGACGGGGAGGGCAAGATCGTGGCGG 493  
Qy 340 GCGCGGGAGAGCAGCACTTCTCGCCAAAGAAACACCAAGCGCGCAAGAGGCTCTCGA 399  
Db 492 GCGCGGGAGAGCAGCACTTCTCGCCAAAGAAACACCAAGCGCGCAAGAGGCTCTCGA 433  
Qy 400 AGATGTGCAAGTCAACAAGAGTGATACGACAAATGTTACGGGTGCACTGCCCTAC 459  
Db 432 AGATGTGCAAGTCAACAAGAGTGATACGACAAATGTTACGGGTGCACTGCCCTAC 373  
Qy 460 AAGTGAATAGGAAGCAAACTGAGAGCTACGTGGTCTTCAAAAAATCATTAAGTTTCG 519  
Db 372 AAGTGAATAGGAAGCAAACTGAGAGCTACGTGGTCTTCAAAAAATCATTAAGTTTCG 313  
Qy 520 CCACCAAAATGTAATTTGTGTATCTTCCACTGTATTTCTTCAAAAAATCTAGAGCA 579  
Db 312 CCACCAAAATGTAATTTGTGTATCTTCCACTGTATTTCTTCAAAAAATCTAGAGCA 253  
Qy 580 TCATTTCAAGCAAGCAAAAAACAATCTCTGGTATCAACAGTATAGCGATATTTCA 639  
Db 252 TCATTTCAAGCAAGCAAAAAACAATCTCTGGTATCAACAGTATAGCGATATTTCA 193  
Qy 640 GAGTGCACTGCTTGTATATAGTTGTTATTTAGTCGCAAAATATGCAAGTGAAGTG 699  
Db 192 GAGTGCACTGCTTGTATATAGTTGTTATTTAGTCGCAAAATATGCAAGTGAAGTG 133  
Qy 700 CTTGAGCCATTAGCTCTCTTAGGATATGCCAGCAGATCGTGTATATGGCTGTGCAAGA 759  
Db 132 CTTGAGCCATTAGCTCTCTTAGGATATGCCAGCAGATCGTGTATATGGCTGTGCAAGA 73  
Qy 760 CACTGTTTGCACCATTTATATATAGCTGCAATGTTTACATGATGAAGCTTGAATAG 819  
Db 72 CACTGTTTGCACCATTTATATATAGCTGCAATGTTTACATGATGAAGCTTGAATAG 14  
Qy 820 GATATGG 826  
Db 13 GATATGG 7

RESULT 4  
AI001298  
LOCUS  
DEFINITION  
AI001298  
MEST6-D3. TWI412. Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA  
sequence.